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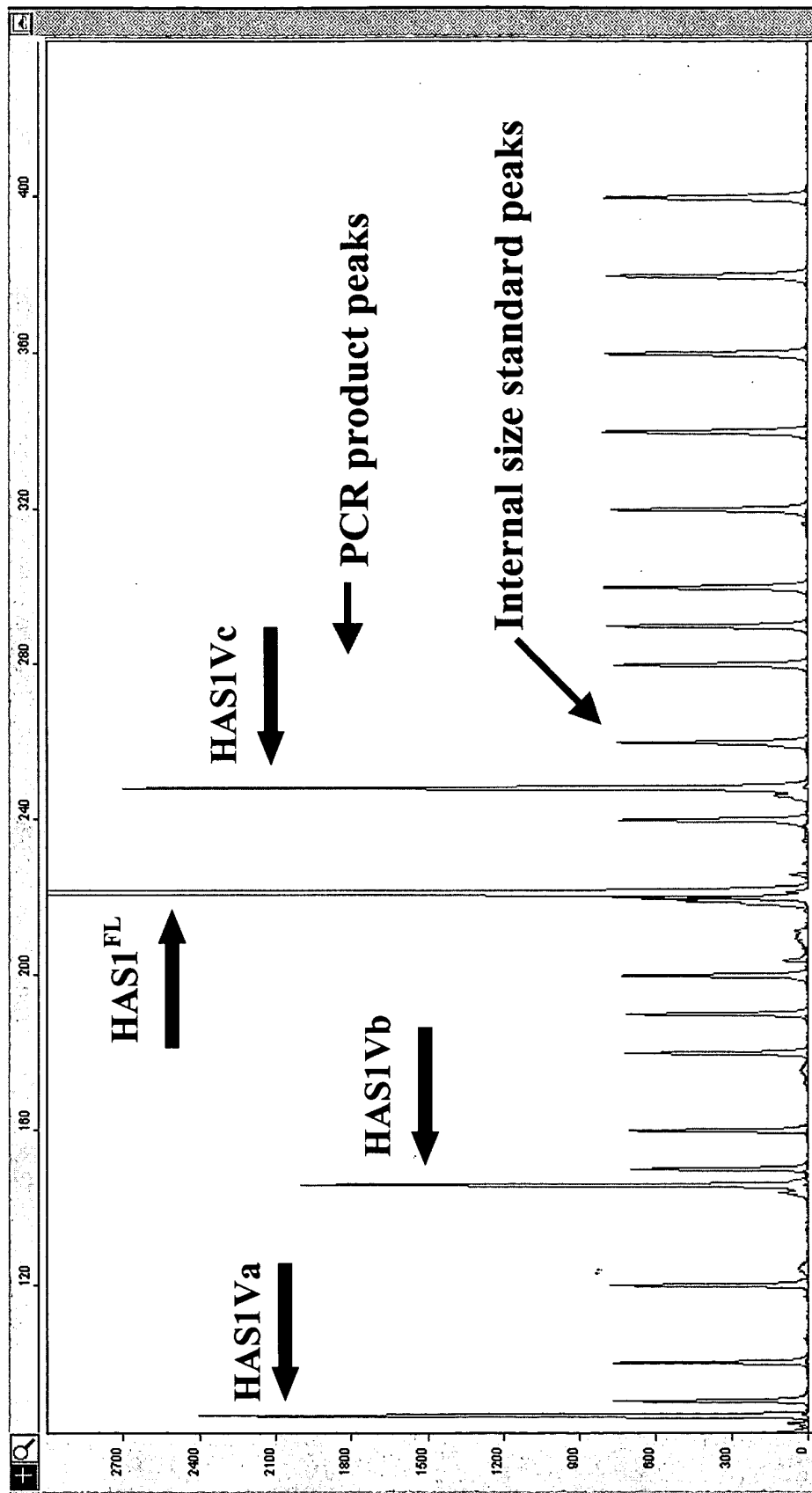
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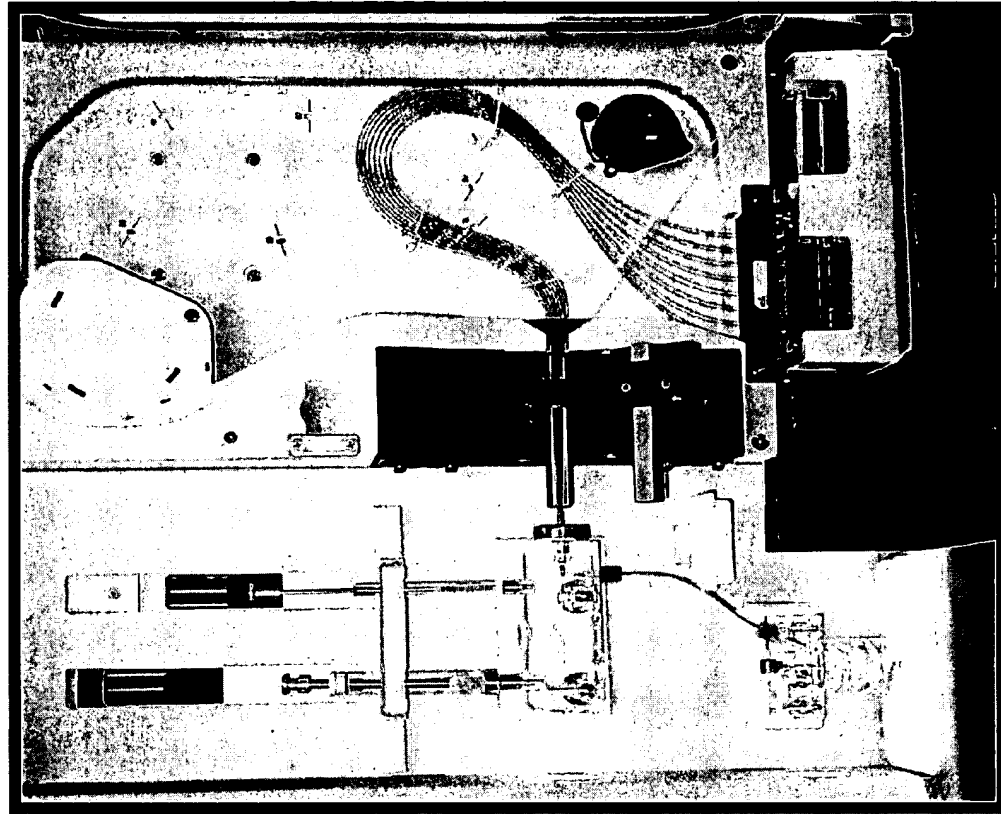
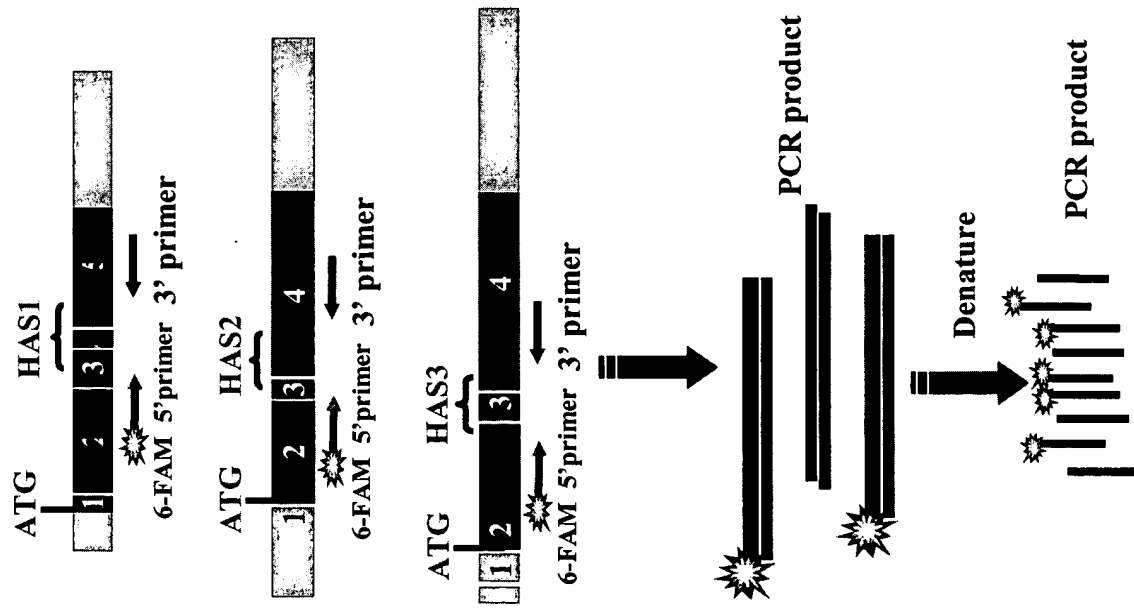


FIG 1



RFU- Relative Fluorescent Units

FIG 2



3100 Genetic Analyzer

FIG 3A

The x-axes represent molecular size (bp) of PCR product and the y-axes Relative Fluorescent units (RFU). — internal size standard peaks; — PCR product peaks.

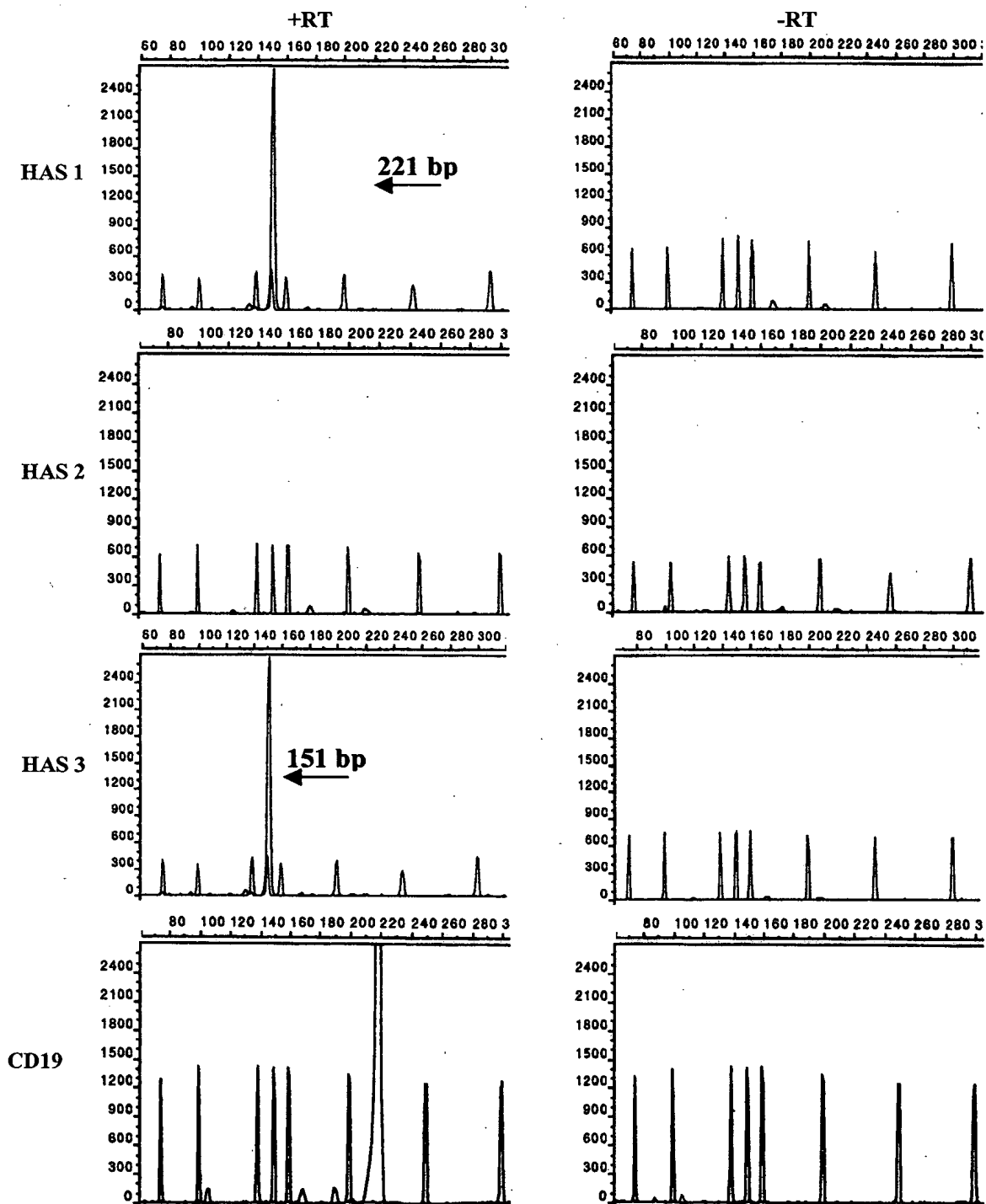


FIG 3B

The x-axes represent molecular size (bp) of PCR product and the y-axes Relative Fluorescent units (RFU). — internal size standard peaks; — PCR product peaks.

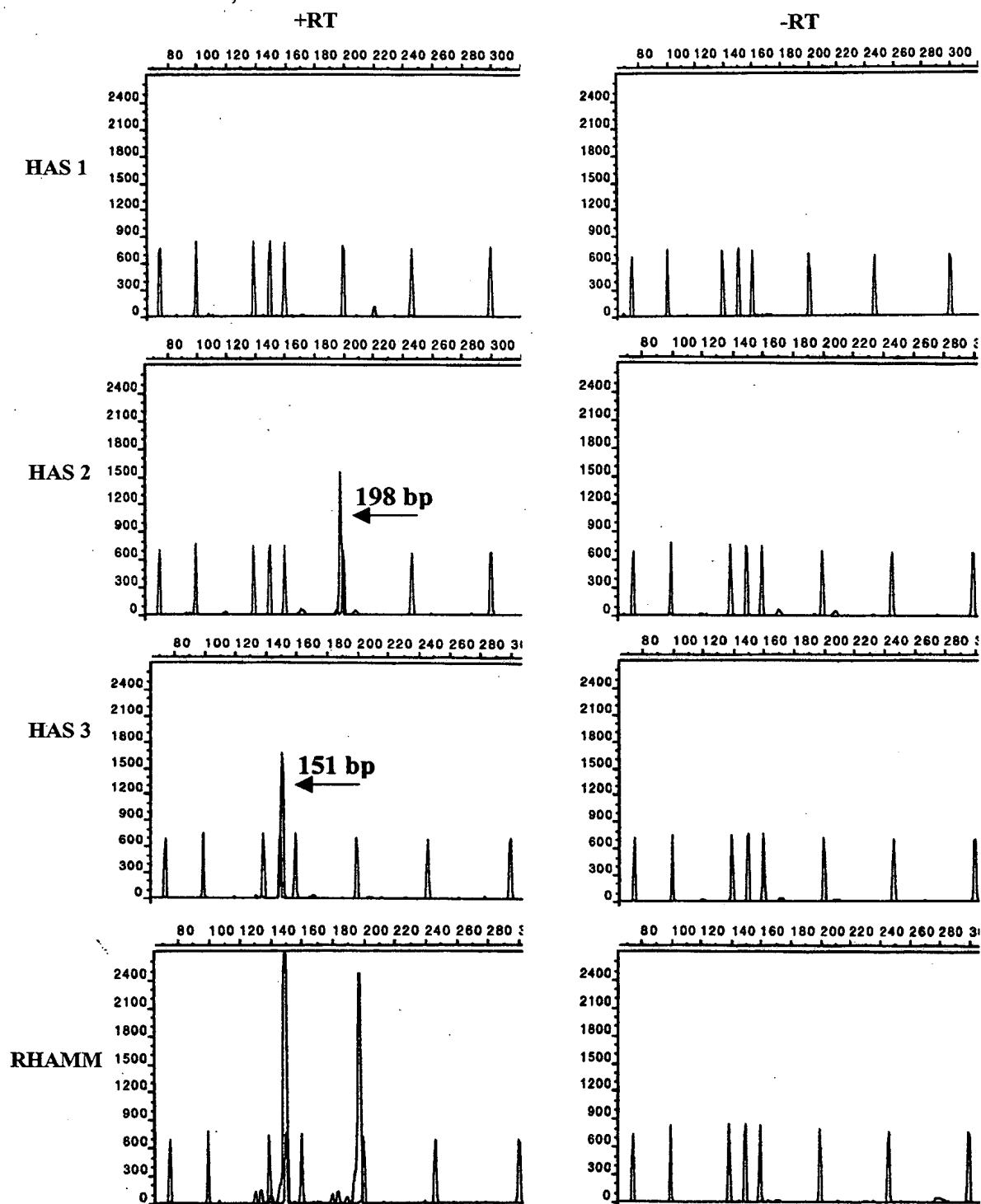


FIG 4A

MM B cells 48h after culturing

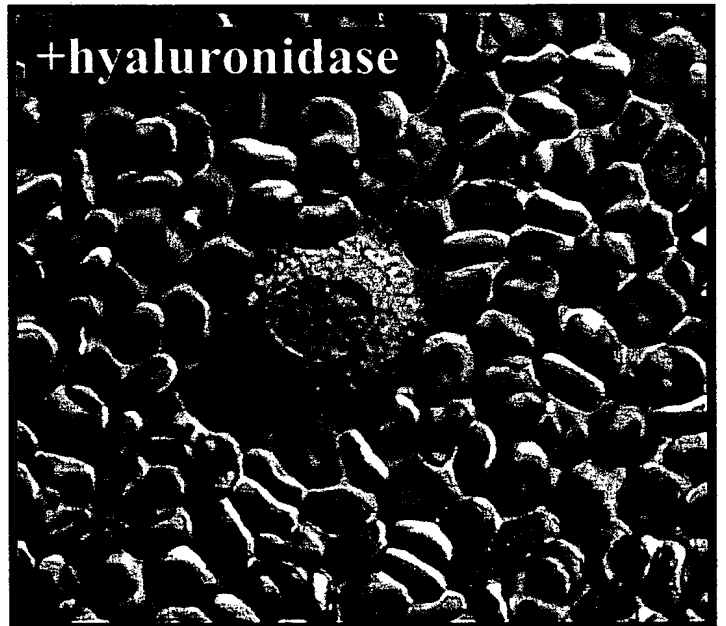
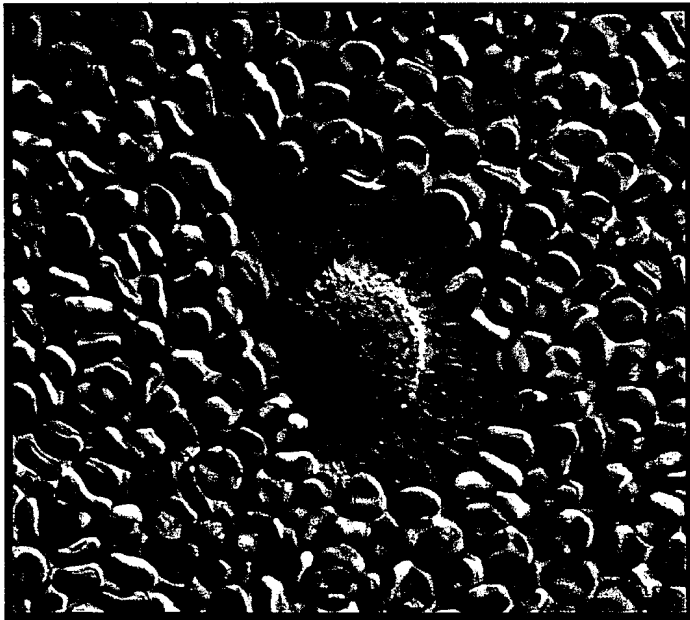
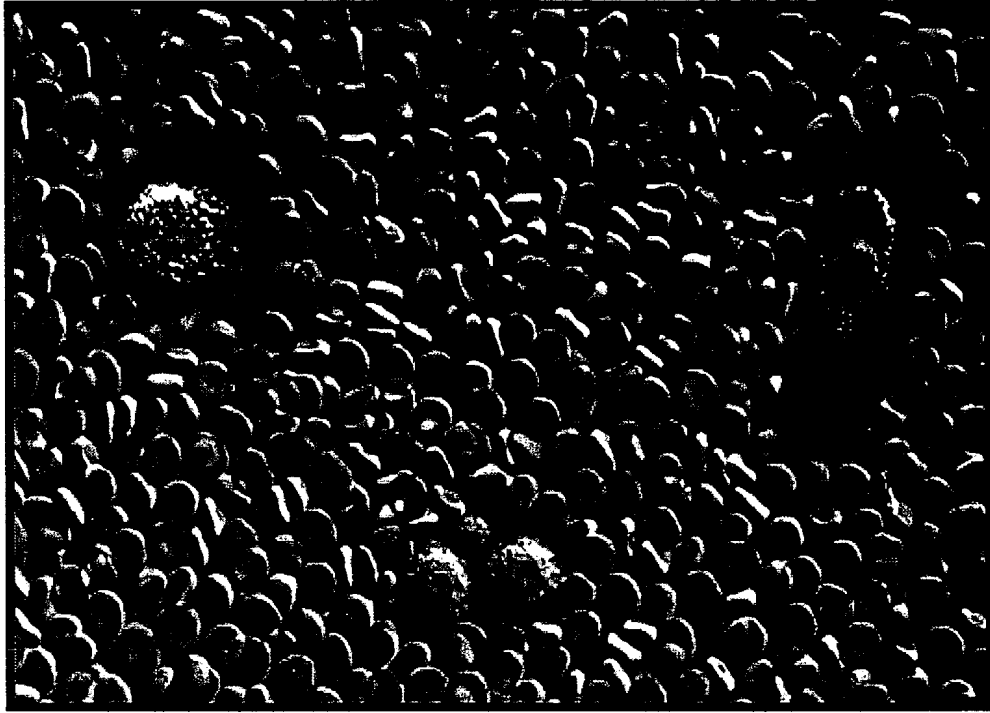


FIG 4B

Particle Exclusion Assay in combination with HA staining



MM B 48h after culturing

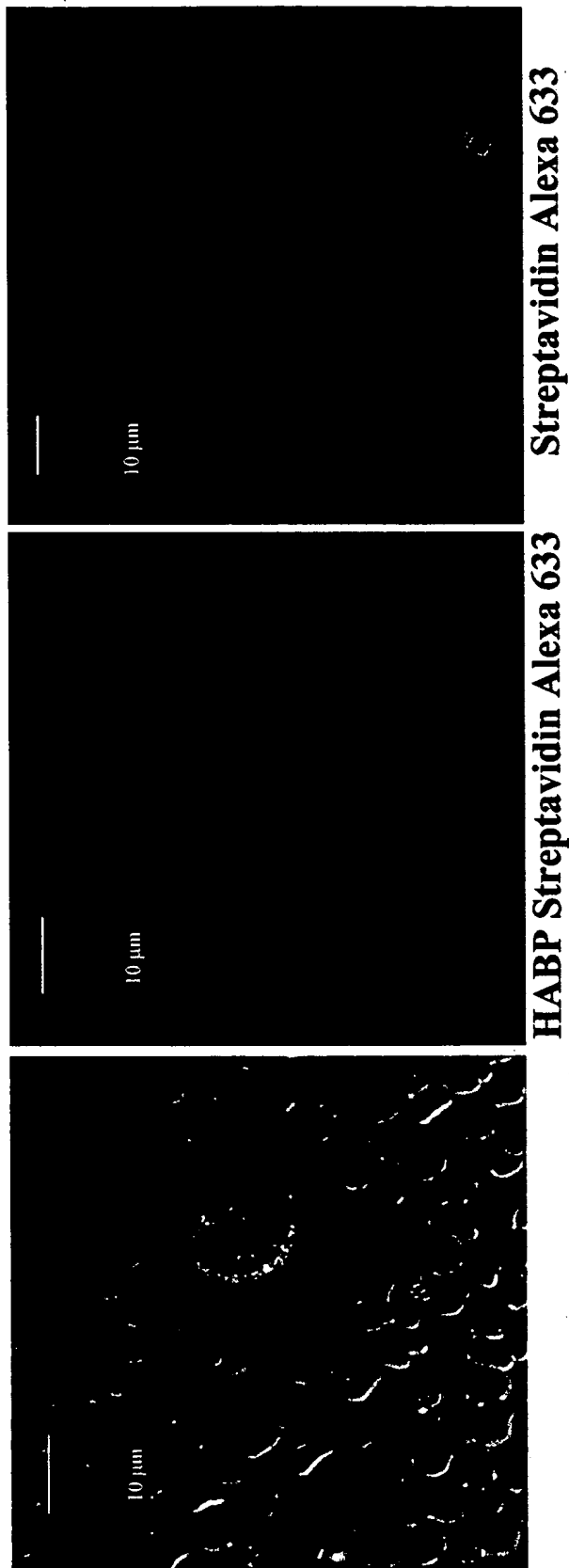
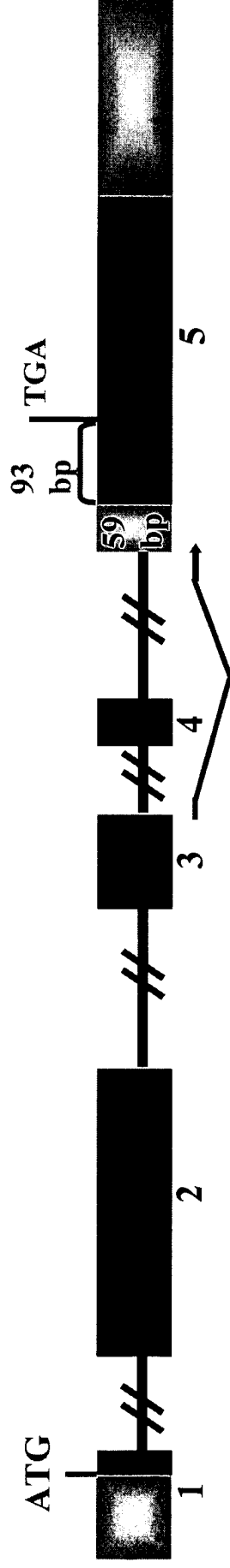


FIG 5B

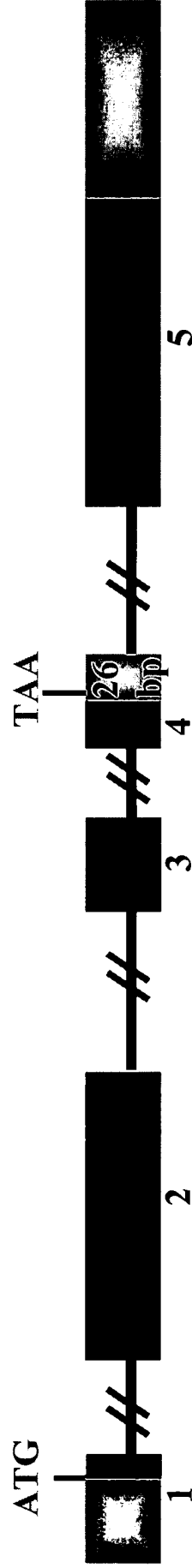
HAS 1Vb



HAS 1Vb - 361 aa - 39.52 KD

FIG 5C

HAS 1Vc



HAS 1Vc - 354/381 aa - ~36 KD

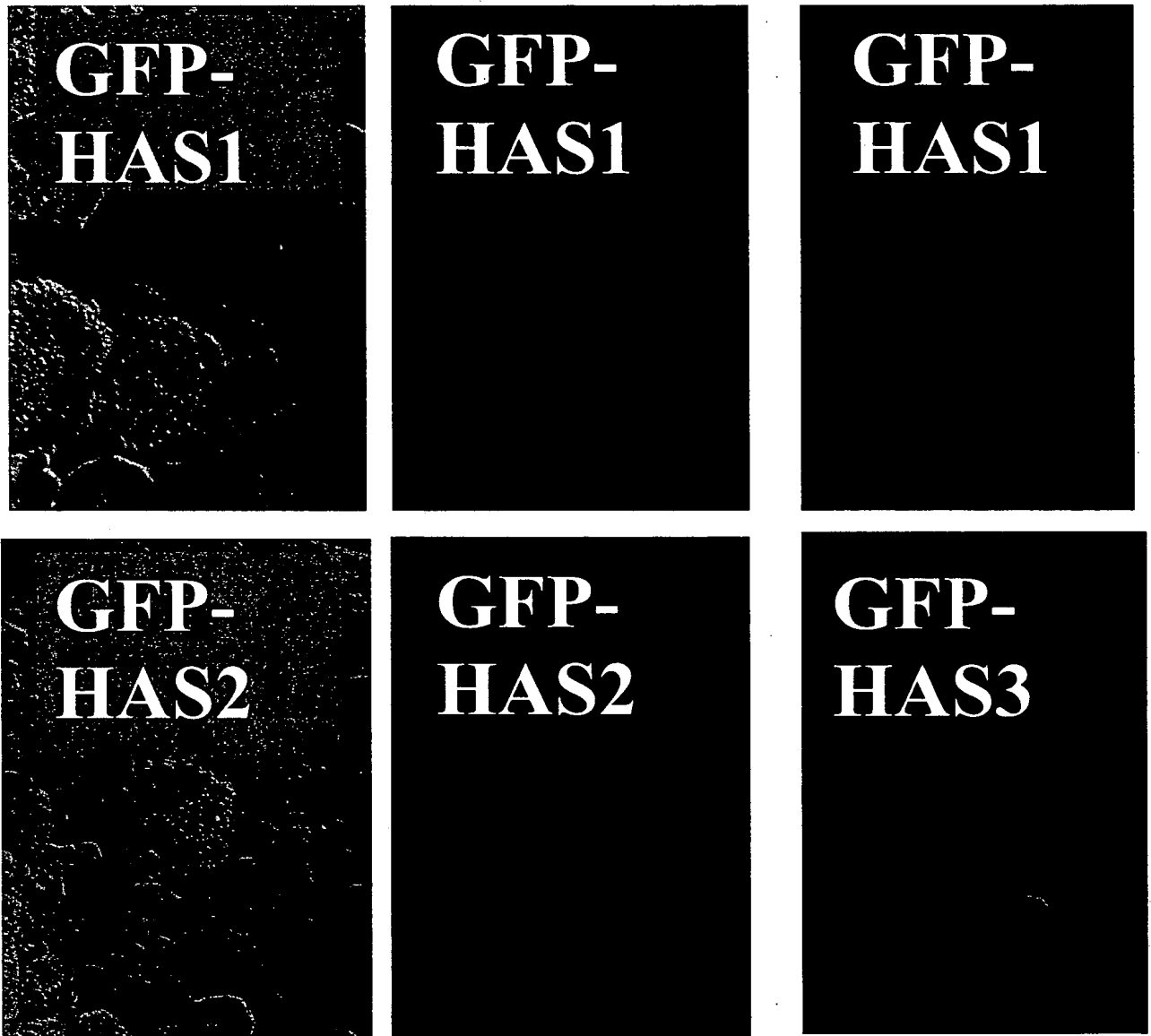
FIG 6

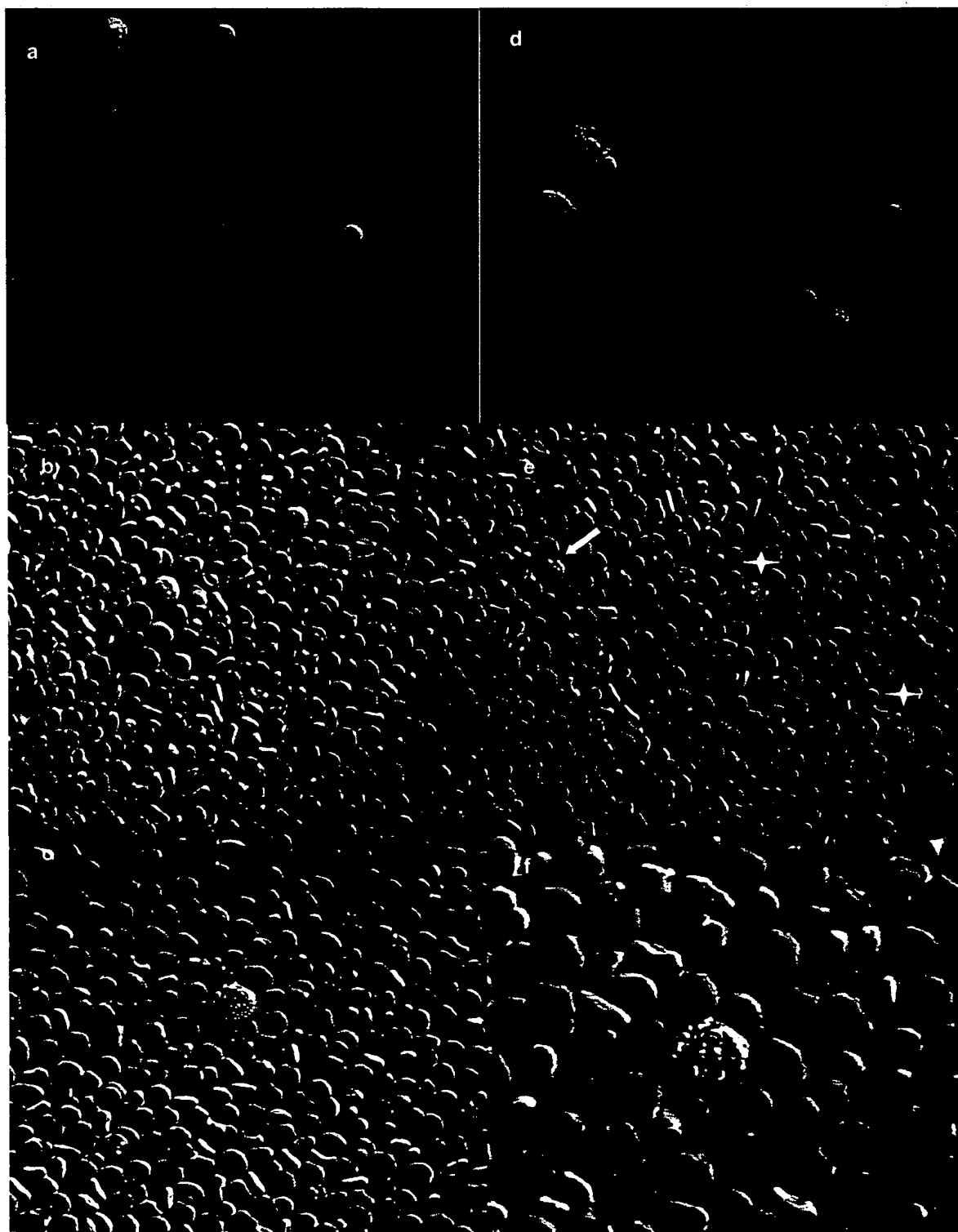
FIG 7

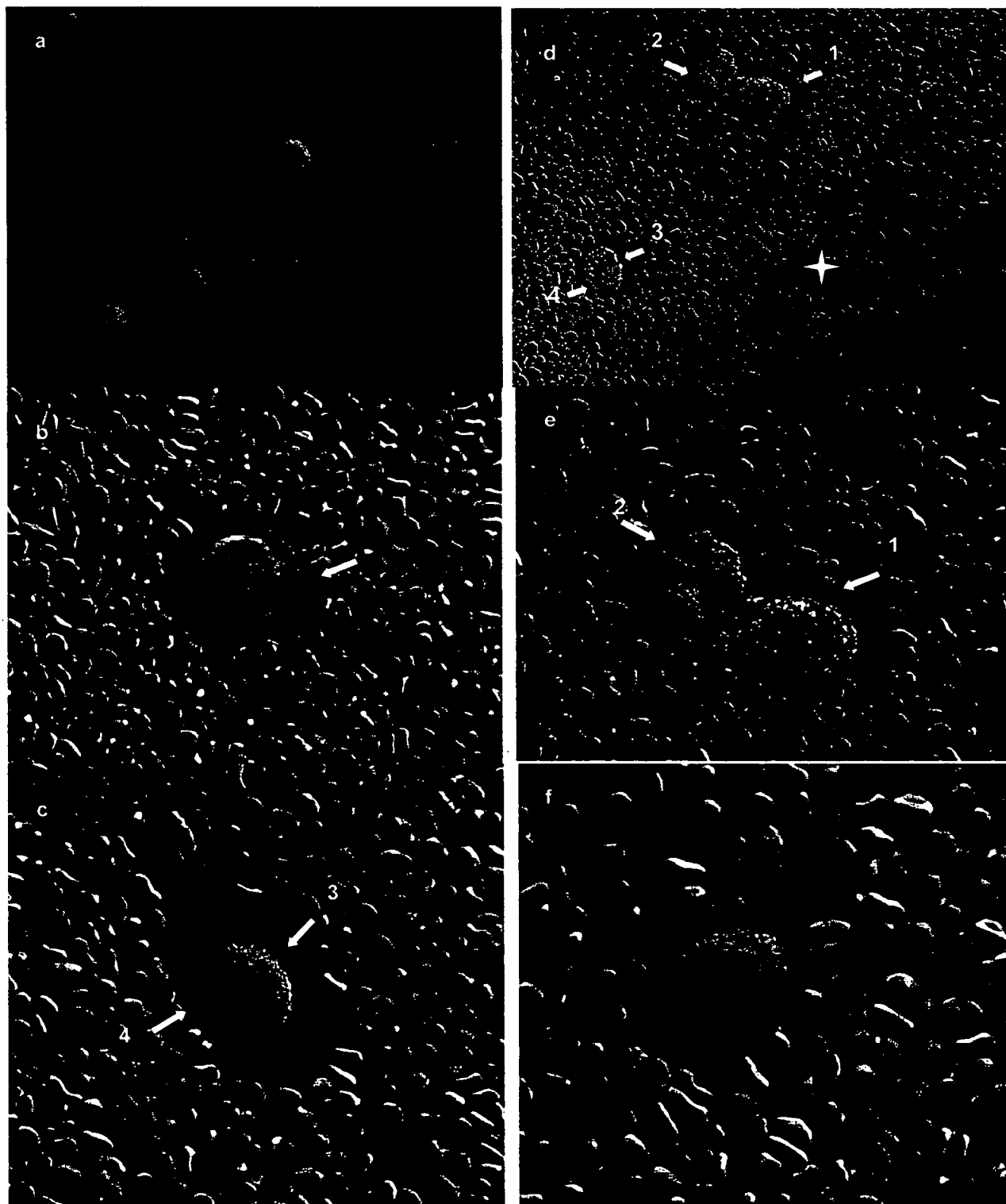
FIG 8

FIG 9

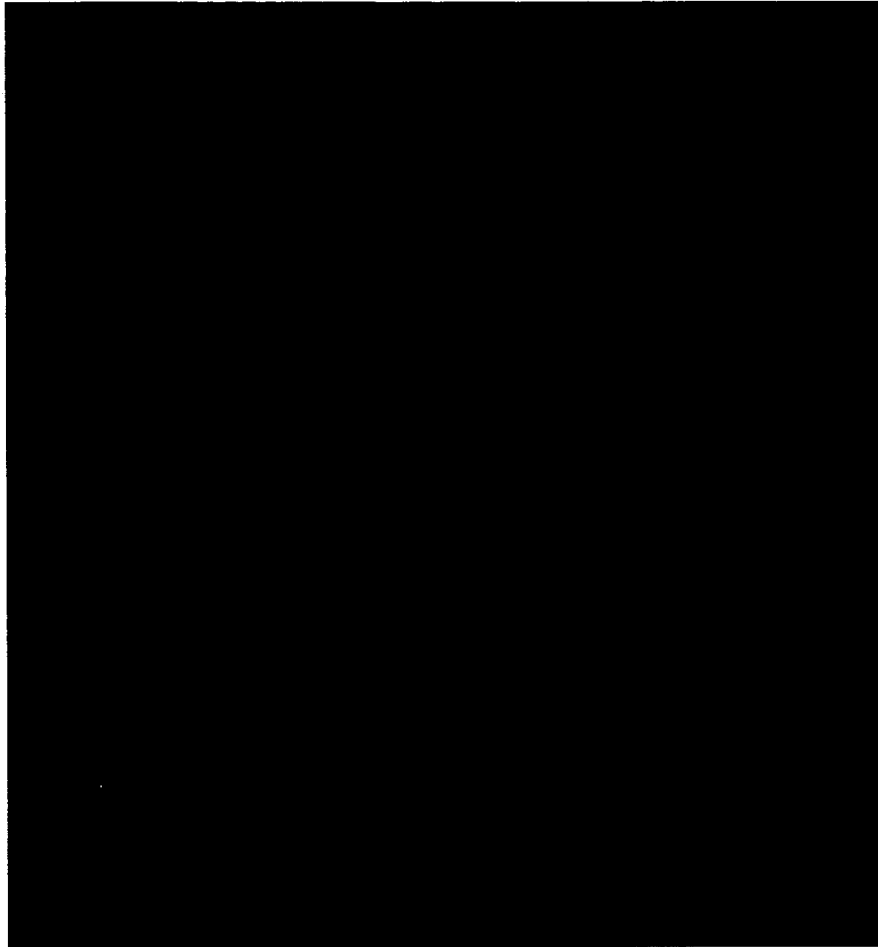
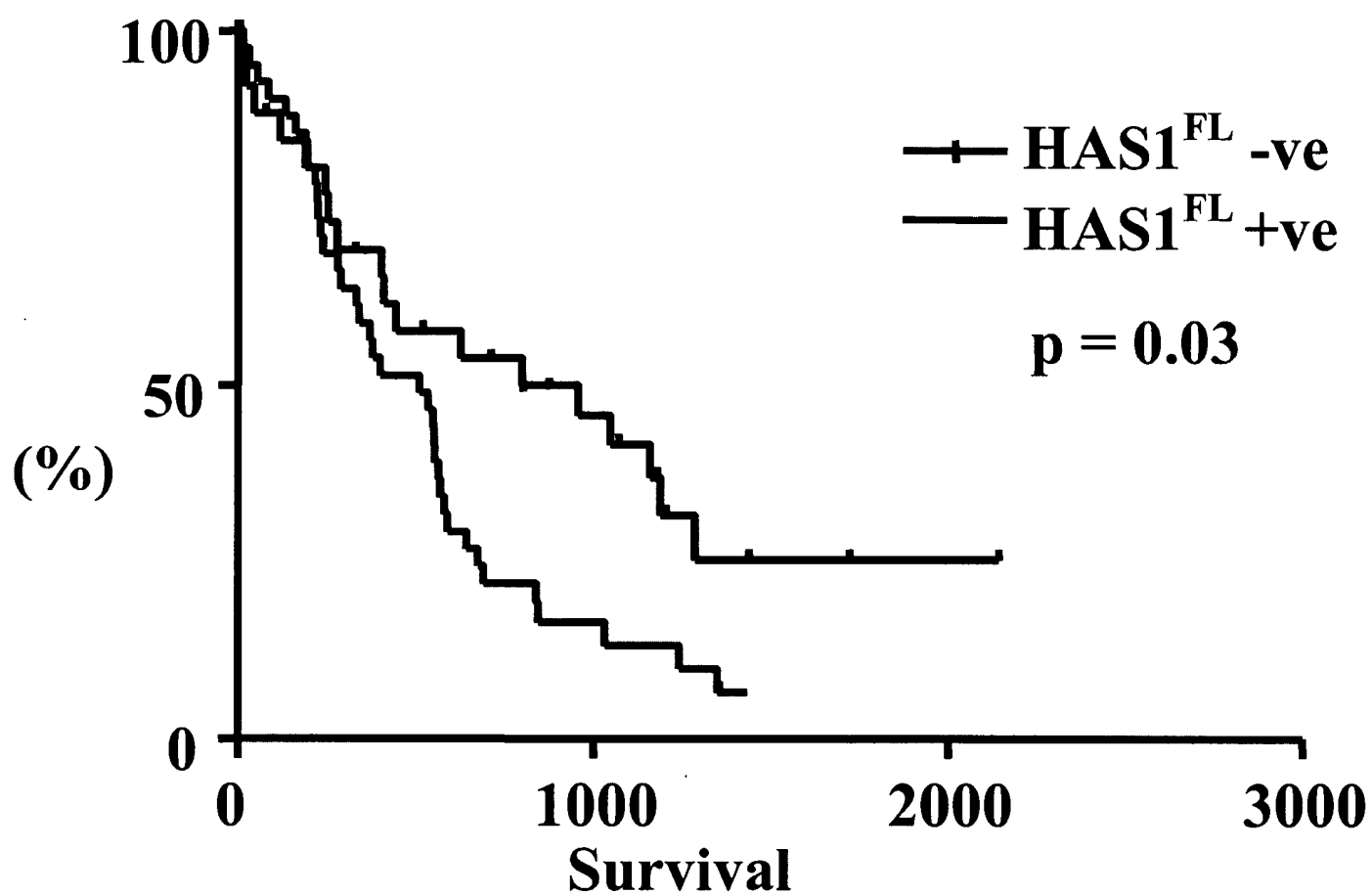


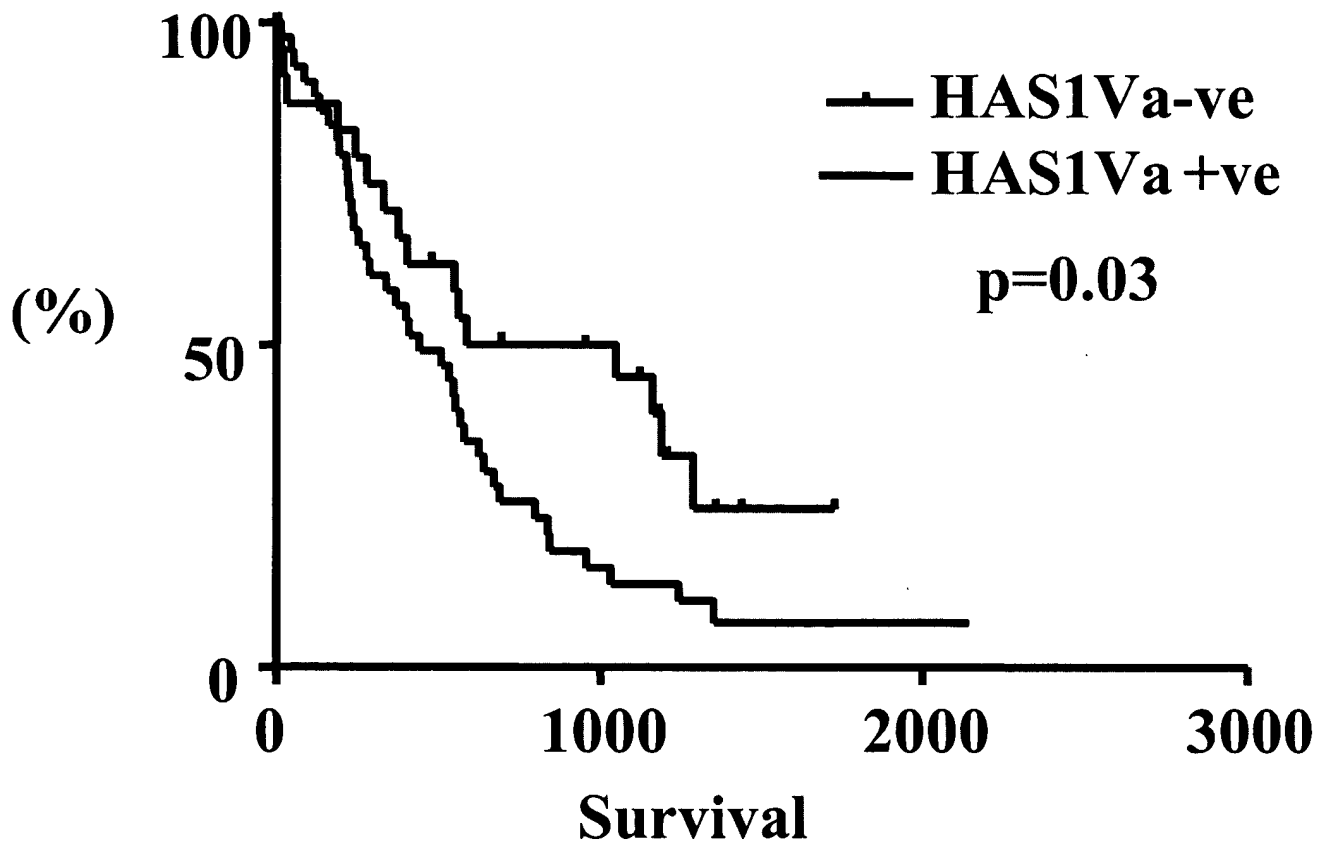
FIG 10

Overall Survival- HAS1^{FL}



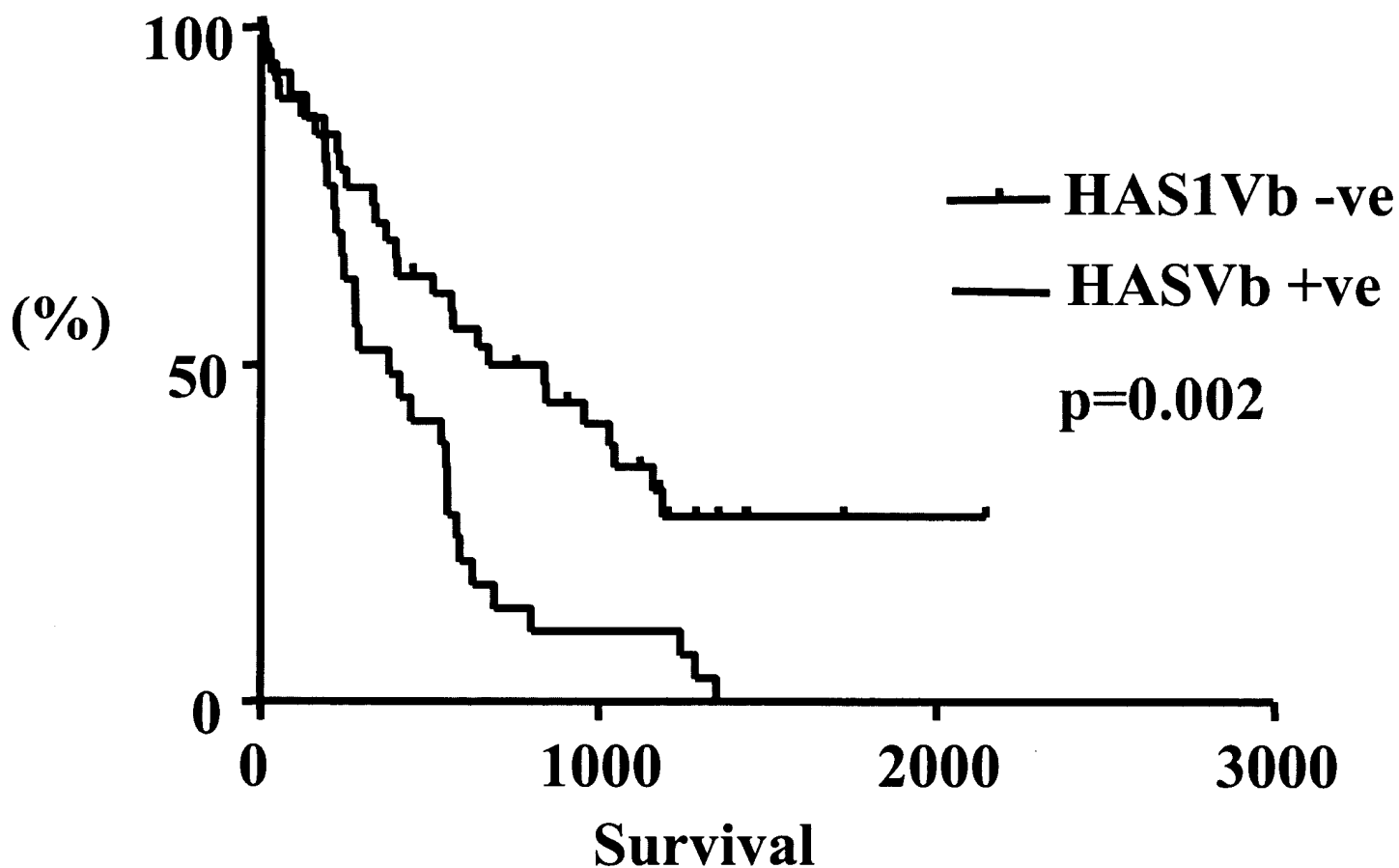
Kaplan-Meier survival plots for patients with Multiple Myeloma. $p=0.03$, using the log rank test.

FIG 11

Overall Survival- HAS1Va

Kaplan-Meier survival plots for patients with Multiple Myeloma. $p=0.03$, using the log rank test.

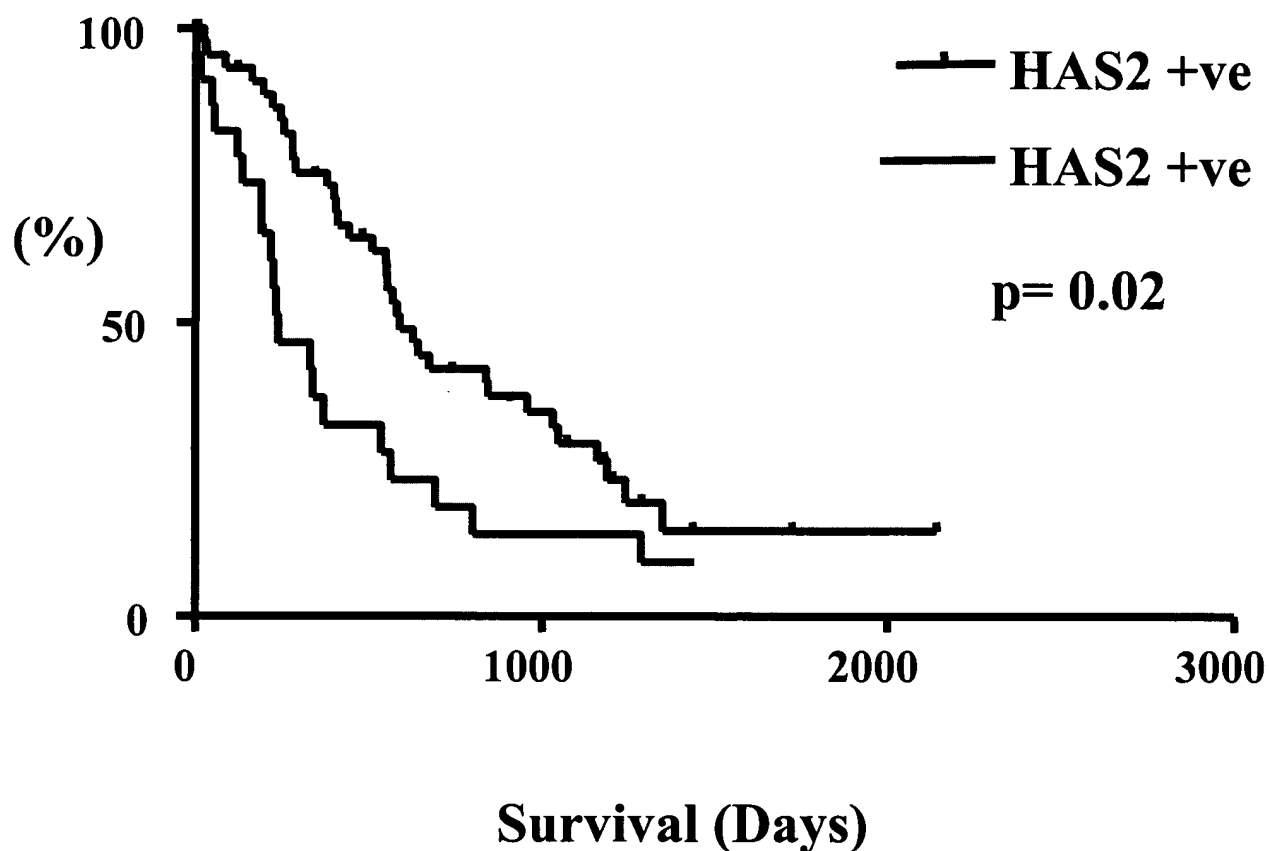
FIG 12

Overall Survival- HAS1Vb

Kaplan-Meier survival plots for patients with Multiple Myeloma. $p=0.002$, using the log rank test.

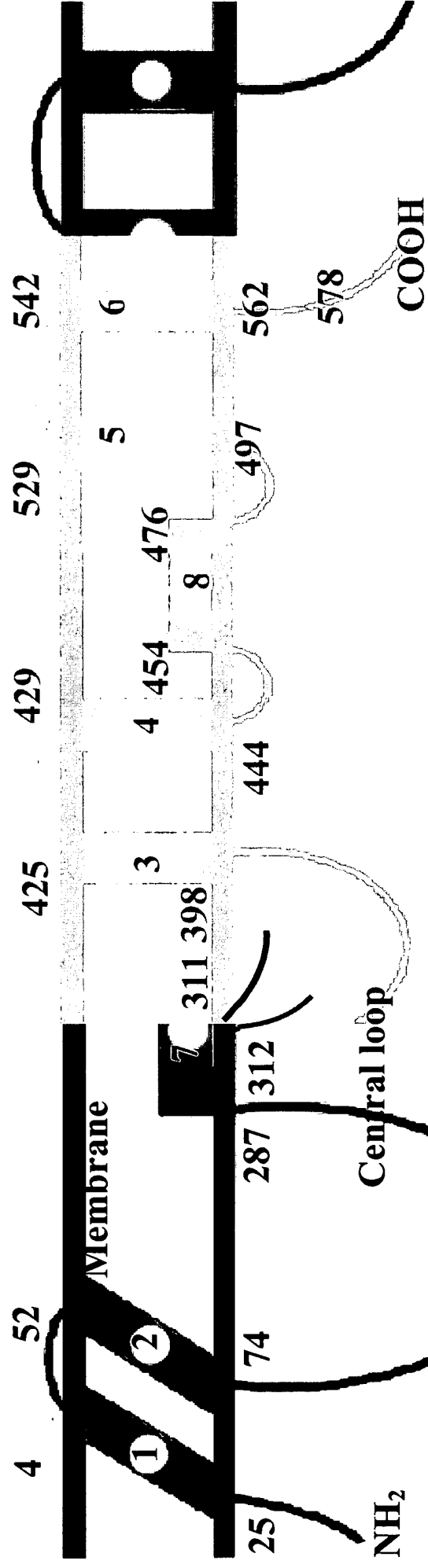
FIG 13

Overall Survival - HAS2



Kaplan-Meier survival plots for patients with Multiple Myeloma. $p=0.02$, using the log rank test.

FIG 14



204-321aa - Glycosyl transferase 231-382aa - Chitin

Weigel, 1997; Heldermon et al., 2001

FIG 15

Secondary mRNA structure predicted

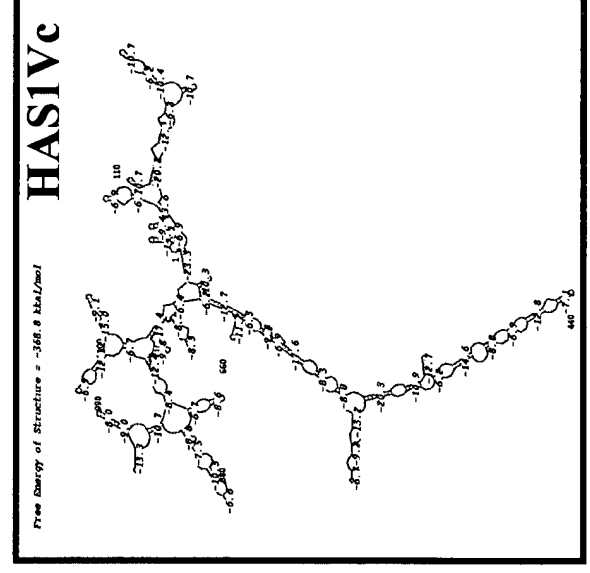
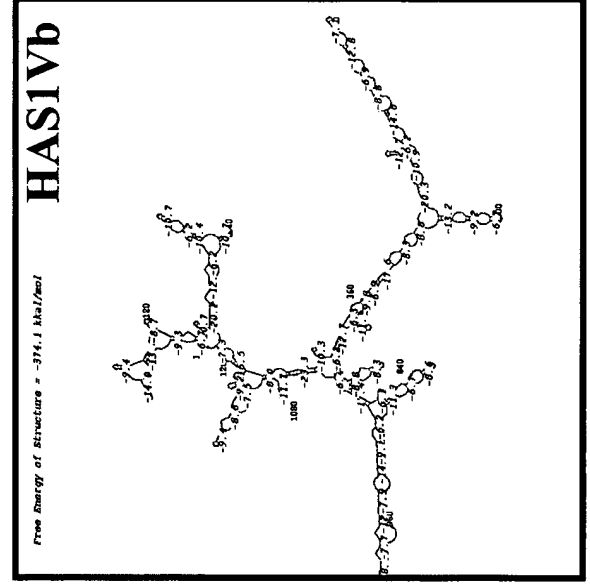
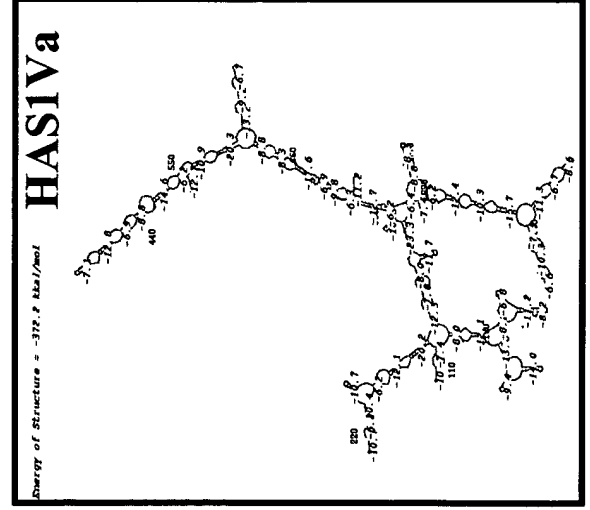
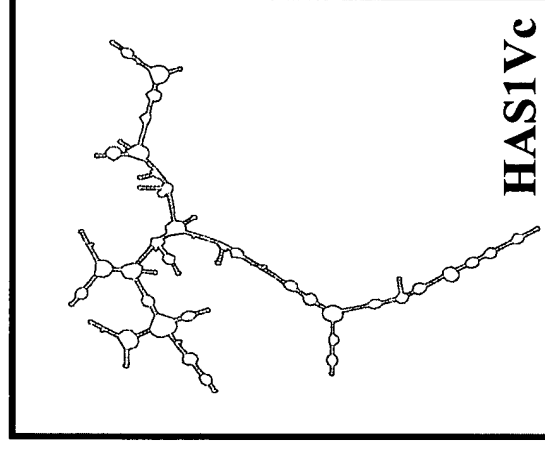
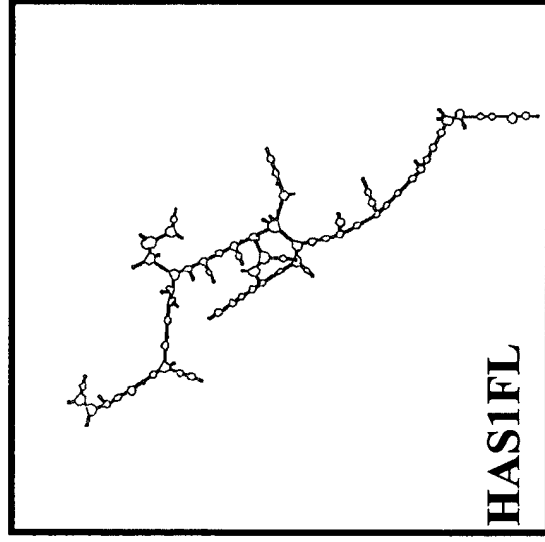


FIG 16

RT-PCR product analysis on microfluidic chip.

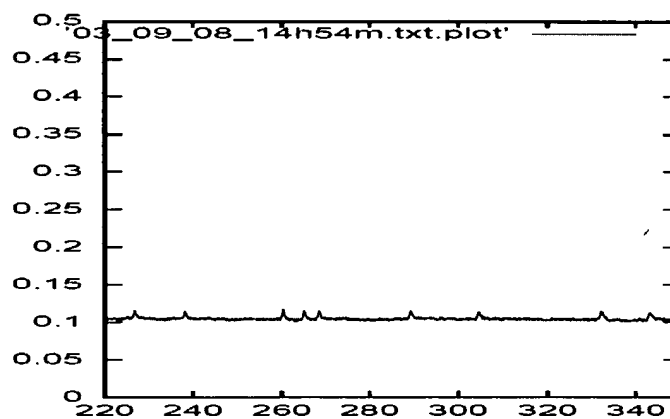
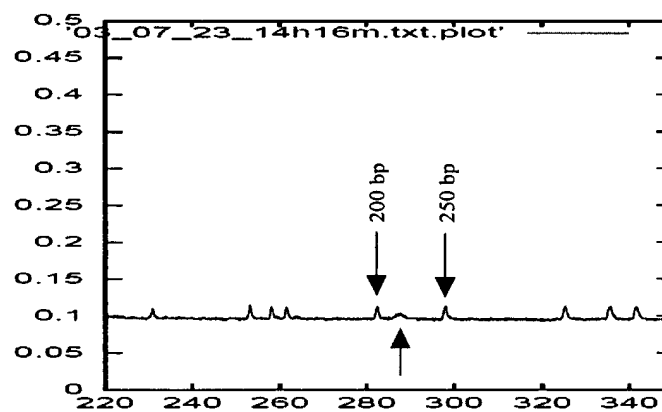
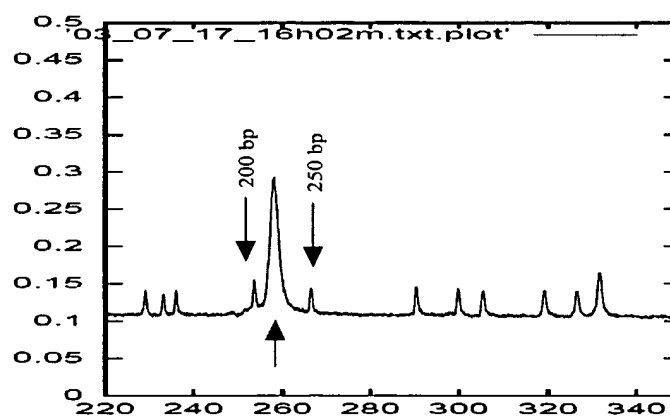
**Negative
Control****15 cycles****20 cycles**

FIG 17

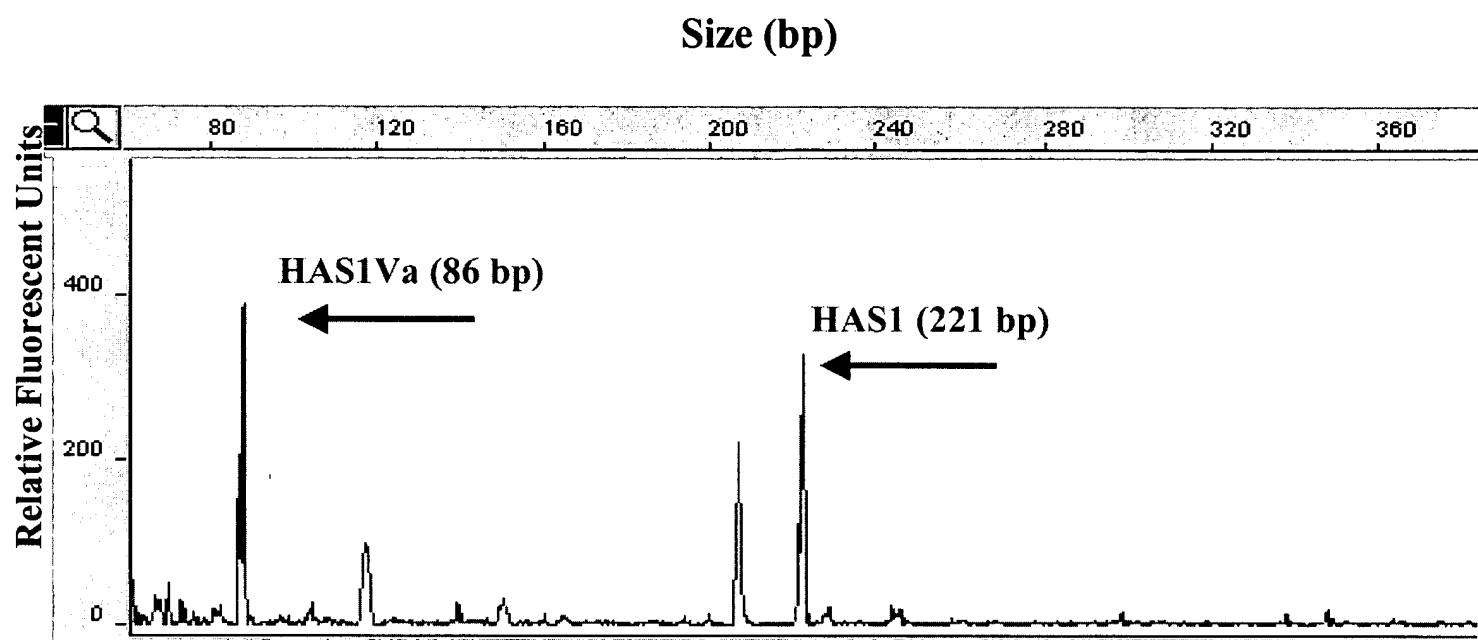


FIG 18

splice sites on intron 4 (fragment)

1	taagctgag gggaccagggt ggtcggat gtgtggaggc caatgaatat cctagcgtgt gtgcatgctg agagtctctcc aaatccaaag
91	taactcacca gacaatgggc tctatcaagt gagacttttag agggagagagg aggtataccat aatggggcaga gggggccattt gcattgagcc
181	aatggactct accaagttag atattaggga agaggggaag atactataag ggacaaggct ggcatttgca ttgaaccatg gaatgcggtg
271	aactctacca agagaggcaa gaggggta pagaaattcca cctagaattg agataggag agttgggtct gtcatggaga ccaaggtagc
361	acagtggga gtgaagttag aagggcaaga gacaaatgga tagagtggga tctaactagt gagagagcca cggagagaa aacaagttag
451	agaagaggag cacctgaact ctaaaagtt cttcaagaga agacaagtaa ttccatgaga ctcaaggagg gatgatctag accaagtga
541	gttcagggga gagtgatctc tgcaaaagcca ggtccactga aatacccaga ggaacttgg gataatccag gggaaatccat gcattaatc
631	actcaacaaa tattcactag gtgcctagaa tgtttaagct gcgggggatac agcaataggc agacaggaca ccaattgatt acatcagttg
721	gggagacaca caagaaaataa ataagtagaa catacagtat gtccatgata tgtgttatyg agataaataa tgccggggcaa ggytgytgga
811	taggaagttt tggggttggg ggtgaagtgt taagtggagt gcctgagaa ggatggggct caaggctgag aatagtgtgg ctgggagcact
901	gaactggggg agtattagga gaggagatg gagagttaag gagtgggtcca ctcatgaaag gcttataggt ctaagggactc tgactaaagt
991	gagggagcca tgggagggtt ttaagcagag aagtgcacg ttgtaatggg atccctctyg cagccgtttt gggtagacagac tacaaaaaggc
1081	aaggtcggaa gcagggaggc cactgaggat gccaaagtgc acagggggaag gagtctggac actgtcaaagt aatgccccagg atctctctct
1171	tgtgtgggct tggctggaaa ccatgcaggg attgattaat gatgtctgcc acaaaacagg aaggagggcct gatgggtccc ttgagaagtt
1261	ctaatacata gactaccctg ggtagcaacc acaccatct tgctcctccc tatagggcct gccagtaata aagcatgg tagtattagt
1351	aatatgttag tgatagtatt agtaatagg tcagtaacca acatgatatt agtaacagca atagtaatgg taacagcaat agtcatagta
1441	aaaacggtag tagctaacat ttattgagca aatactatct actgggtccta agcacttggc gttaaatttc attcaatcct tacaggtatcc
1531	ttgtcttatg agagcctttt tttttttctt agatatagagtc ttgctgtgtt gctcaggctc ccaaatagct gggaggggac gatcatggct
1621	cactgcagcc tcaaaactcct gagctcaagt gattccccca tctcagcctc ccaaatagct gggactacag gccaccacgc ccggctaatt
1711	ttttttttt tttttttttt ttagagatgg ggtctcacta tgttgcttag gctgatctca aactcttagc ctcaagtgat cccctacct
1801	cagcctccta aagtgtctggg attacaggca tgaagcattg catcccaccc attggtgctt atttatttat ttattttatt atttagtagg
1891	gatgggggtct tgctatgttg cccaggctgg tcttgaactc cttatccctc agcctcccaa agtgctggga ttacaggagt gagccaccgc
1981	gtccaggcct aggaaccatt atccacccta ttctacacat gagaacactg aggcctagag aggttaagaa actcgcccc agtgccgctc
2071	cacagtgttc atttctgctt ccagg

■ donor splice sites (7) score (0.96-0.98) ■ acceptor splice sites (5) score (0.98-1)